NCBI

●●●●   ●● ●   ●○   °○   ●●●●   Entrez Protein

PubMed   Nucleotide   Protein   Genome   Structure   PMC   Taxonomy   OMIM   Boo

Search |Nucleotide ▼| for [_____] |Go| |Clear|

Limits   Preview/Index   History   Clipboard   Details

Display |default ▼| Show: |1 ▼| Send to |File ▼| |Get Subsequence|

☐ 1: BAB82497. scavenger recepto...[gi:18146952]   BLink, Domains, Links

```
LOCUS       BAB82497                 742 aa            linear   ROD 18-JAN-2002
DEFINITION  scavenger receptor with C-type lectin [Mus musculus].
ACCESSION   BAB82497
VERSION     BAB82497.1  GI:18146952
DBSOURCE    accession AB038519.1
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Nakamura,K., Funakoshi,H., Tokunaga,F. and Nakamura,T.
  TITLE     Molecular cloning of a mouse scavenger receptor with C-type lectin
            (SRCL)(1), a novel member of the scavenger receptor family
  JOURNAL   Biochim. Biophys. Acta 1522 (1), 53-58 (2001)
  MEDLINE   21575692
   PUBMED   11718900
REFERENCE   2  (residues 1 to 742)
  AUTHORS   Nakamura,K. and Nakamura,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-FEB-2000) Kenji Nakamura, Osaka University Medical
            School, Division of Biochemistry, Biomedical Research Center; 2-2
            yamadaoka, Suita, Osaka 565-0871, Japan
            (E-mail:knakamur@onbich.med.osaka-u.ac.jp,
            Tel:81-6-6879-3783(ex.3783), Fax:81-6-6879-3789)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:10090"
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      181 lqqdtnvlqg nlqsqmysqs vvimnlnnln ltqvqqrnli snlqqsvddt slaiqriknd
      241 fqnlqqvflq akkdtdwlke kvqslqtlaa nnsalakann dtledmnsql ssftgqmdni
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//

Mar 17 2003 10:55:57

NCBI **Blast 2 Sequences results**

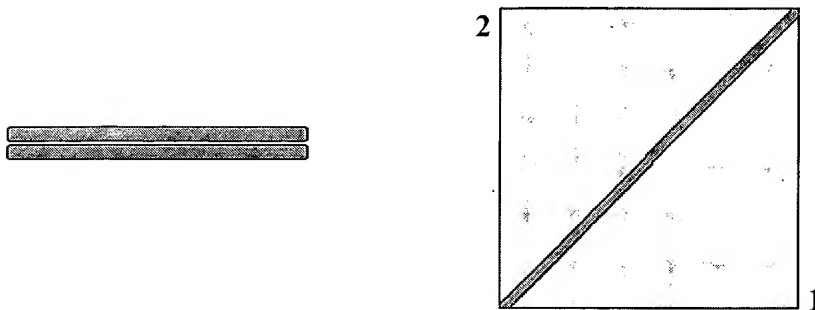PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.5 [Nov-16-2002]

Matrix [BLOSUM62 ▼] gap open:[11] gap extension: [1]

x_dropoff: [50] expect:[300.0] wordsize: [3] Filter ☐ [Align]

Sequence 1 gi 17026101 collectin placenta 1 [Homo sapiens]   **Length** 742 (1 .. 742)

Sequence 2 gi 18146952 scavenger receptor with C-type lectin [Mus musculus] **Length** 742 (1 .. 742)

NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

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Identities = 680/742 (91%), Positives = 717/742 (95%)
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Query: 361  TSNLNEVRTTCTDTLTKHTDDLTSLNNTLANIRLDSVSLRMQQDLMRSRLDTEVANLSVI 420
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Sbjct: 421 MEEMKLVDSKHGQLIKNFTILQGPPGPRGPKGDRGSQGPPGPTGNKGQKGEKGEPGPPGP 480

Query: 481 AGERGPIGPAGPPGERGGKGSKGSQGPKGSRGSPGKPGPQGPSGDPGPPGPPGKEGLPGP 540
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Query: 541 QGPPGFQGLQGTVGEPGVPGPRGLPGLPGVPGMPGPKGPPGPPGPSGAVVPLALQNEPTP 600
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Query: 601 APEDNGCPPHWKNFTDKCYYFSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVG 660
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Query: 661 RESHWIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDCAGLIYAGQWNDF 720
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Query: 721 QCEDVNNFICEKDRETVLSSAL 742
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   0.311    0.132    0.391

Gapped
Lambda      K        H
   0.267    0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 19,527
Number of Sequences: 0
Number of extensions: 530
Number of successful extensions: 99
Number of sequences better than 300.0: 1
Number of HSP's better than 300.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 742
length of database: 455,821,981
effective HSP length: 135
effective length of query: 607
effective length of database: 455,821,846
effective search space: 276683860522
effective search space used: 276683860522
T: 9
A: 40
X1: 16 ( 7.2 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 42 (21.8 bits)
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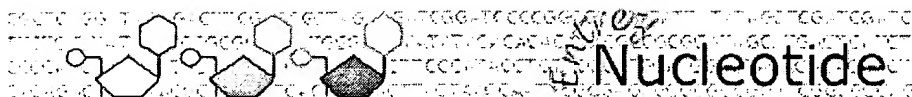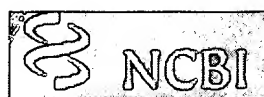
S2: 66 (30.0 bits)

NCBI

| PubMed | Nucleotide | Protein | Genome | Structure | PMC | Taxonomy | OMIM | Boo |

Nucleotide

Search | Nucleotide ▼ | for [   ] | Go | Clear |

Limits   Preview/Index   History   Clipboard   Details

| Display | default ▼ | Show: | 20 ▼ | Send to | File ▼ | Get Subsequence |

☐ 1: AB005145. Homo sapiens CL-P...[gi:17026100]   Links

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LOCUS       AB005145                2983 bp    mRNA    linear   PRI 21-NOV-2001
DEFINITION  Homo sapiens CL-P1 mRNA for collectin placenta 1, complete cds.
ACCESSION   AB005145
VERSION     AB005145.1  GI:17026100
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ohtani,K., Suzuki,Y., Eda,S., Kawai,T., Kase,T., Keshi,H.,
            Sakai,Y., Fukuoh,A., Sakamoto,T., Itabe,H., Suzutani,T.,
            Ogasawara,M., Yoshida,I. and Wakamiya,N. — Regist in
  TITLE     The membrane-type collectin CL-P1 is a scavenger receptor on
            vascular endothelial cells
  JOURNAL   J. Biol. Chem. 276 (47), 44222-44228 (2001)
  MEDLINE   21570232
   PUBMED   11564734
REFERENCE   2  (bases 1 to 2983)
  AUTHORS   Ohtani,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUN-1997) Katsuki Ohtani, Asahikawa Medical College,
            Department of Microbiology; 2-1-1-1 Midorigaoka-Higashi, Asahikawa,
            Hokkaido 078-8510, Japan (E-mail:ohtani@asahikawa-med.ac.jp,
            Tel:+81-166-68-2393, Fax:+81-166-68-2399)
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Handwritten annotations:
- "coding Seu" (pointing to line 61)
- "Start Encode SEQ ID:2" (pointing near line 601)
- "End encode SEQ ID:2" (pointing to line 2341 / ~2329)

Mar 17 2003 10:55:57

NCBI   • • •• •●• ●●●• C•▓▒A• • • •   ᵉⁿᵗʳᵉʐ Protein

PubMed   Nucleotide   Protein   Genome   Structure   PMC   Taxonomy   OMIM   Boo

Search [Nucleotide ▼] for [   ] [Go] [Clear]

Limits   Preview/Index   History   Clipboard   Details

Display [default ▼] Show: [1 ▼] [Send to] [File ▼] [Get Subsequence]

☐ 1: BAB39147. scavenger recepto...[gi:13365515]   BLink, Domains, Links

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LOCUS       BAB39147               742 aa            linear   PRI 08-MAR-2001
DEFINITION  scavenger receptor with C-type lectin type I [Homo sapiens].
ACCESSION   BAB39147
VERSION     BAB39147.1  GI:13365515
DBSOURCE    accession AB038518.1
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Nakamura,K., Funakoshi,H., Miyamoto,K., Tokunaga,F. and Nakamura,T.
  TITLE     Molecular cloning and functional characterization of a human
            scavenger receptor with C-type lectin (SRCL), a novel member of a
            scavenger receptor family
  JOURNAL   Biochem. Biophys. Res. Commun. 280 (4), 1028-1035 (2001)
  MEDLINE   21092718
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REFERENCE   2  (residues 1 to 742)
  AUTHORS   Nakamura,K. and Nakamura,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-FEB-2000) Kenji Nakamura, Osaka University Medical
            School, Division of Biochemistry, Biomedical Research Center; 2-2
            yamadaoka, Suita, Osaka 565-0871, Japan
            (E-mail:knakamur@onbich.med.osaka-u.ac.jp,
            Tel:81-6-6879-3783(ex.3783), Fax:81-6-6879-3789)
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721 qcedvnnfic ekdretvlss al
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NCBI Blast 2 Sequences results

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

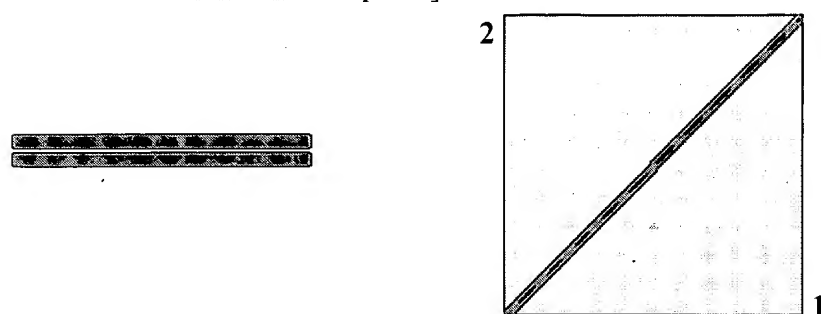## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.5 [Nov-16-2002]

Matrix [BLOSUM62 ▼] gap open:[11] gap extension:[1]

x_dropoff: [50] expect:[300.0(] wordsize:[3] Filter ☐ [Align]

Sequence 1	gi 17026101	collectin placenta 1 [Homo sapiens]	**Length** 742	(1 .. 742)
Sequence 2	gi 13365515	scavenger receptor with C-type lectin type I [Homo sapiens]	**Length** 742	(1 .. 742)

NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

```
Score = 1523 bits (3944), Expect = 0.0
Identities = 741/742 (99%), Positives = 741/742 (99%)
```



```
Query:   1   MKDDFAEEEEVQSFGYKRFGIQEGTQCTKCKNNWALKFSIILLYILCALLTITVAILGYK  60
             MKDDFAEEEEVQSFGYKRFGIQEGTQCTKCKNNWALKFSIILLYILCALLTITVAILGYK
Sbjct:   1   MKDDFAEEEEVQSFGYKRFGIQEGTQCTKCKNNWALKFSIILLYILCALLTITVAILGYK  60

Query:  61   VVEKMDNVTGGMETSRQTYDDKLTAVESDLKKLGDQTGKKAISTNSELSTFRSDILDLRQ  120
             VVEKMDNVTGGMETSRQTYDDKLTAVESDLKKLGDQTGKKAISTNSELSTFRSDILDLRQ
Sbjct:  61   VVEKMDNVTGGMETSRQTYDDKLTAVESDLKKLGDQTGKKAISTNSELSTFRSDILDLRQ  120

Query: 121   QLREITEKTSKNKDTLEKLQASGDALVDRQSQLKETLENNSFLITTVNKTLQAYNGYVTN  180
             QLREITEKTSKNKDTLEKLQASGDALVDRQSQLKETLENNSFLITTVNKTLQAYNGYVTN
Sbjct: 121   QLREITEKTSKNKDTLEKLQASGDALVDRQSQLKETLENNSFLITTVNKTLQAYNGYVTN  180

Query: 181   LQQDTSVLQGNLQNQMYSHNVVIMNLNNLNLTQVQQRNLITNLQRSVDDTSQAIQRIKND  240
             LQQDTSVLQGNLQNQMYSHNVVIMNLNNLNLTQVQQRNLITNL RSVDDTSQAIQRIKND
Sbjct: 181   LQQDTSVLQGNLQNQMYSHNVVIMNLNNLNLTQVQQRNLITNLQRSVDDTSQAIQRIKND  240

Query: 241   FQNLQQVFLQAKKDTDWLKEKVQSLQTLAANNSALAKANNDTLEDMNSQLNSFTGQMENI  300
             FQNLQQVFLQAKKDTDWLKEKVQSLQTLAANNSALAKANNDTLEDMNSQLNSFTGQMENI
Sbjct: 241   FQNLQQVFLQAKKDTDWLKEKVQSLQTLAANNSALAKANNDTLEDMNSQLNSFTGQMENI  300

Query: 301   TTISQANEQNLKDLQDLHKDAENRTAIKFNQLEERFQLFETDIVNIISNISYTAHHLRTL  360
             TTISQANEQNLKDLQDLHKDAENRTAIKFNQLEERFQLFETDIVNIISNISYTAHHLRTL
Sbjct: 301   TTISQANEQNLKDLQDLHKDAENRTAIKFNQLEERFQLFETDIVNIISNISYTAHHLRTL  360
```

```
Query:  361  TSNLNEVRTTCTDTLTKHTDDLTSLNNTLANIRLDSVSLRMQQDLMRSRLDTEVANLSVI  420
             TSNLNEVRTTCTDTLTKHTDDLTSLNNTLANIRLDSVSLRMQQDLMRSRLDTEVANLSVI
Sbjct:  361  TSNLNEVRTTCTDTLTKHTDDLTSLNNTLANIRLDSVSLRMQQDLMRSRLDTEVANLSVI  420

Query:  421  MEEMKLVDSKHGQLIKNFTILQGPPGPRGPRGDRGSQGPPGPTGNKGQKGEKGEPGPPGP  480
             MEEMKLVDSKHGQLIKNFTILQGPPGPRGPRGDRGSQGPPGPTGNKGQKGEKGEPGPPGP
Sbjct:  421  MEEMKLVDSKHGQLIKNFTILQGPPGPRGPRGDRGSQGPPGPTGNKGQKGEKGEPGPPGP  480

Query:  481  AGERGPIGPAGPPGERGGKGSKGSQGPKGSRGSPGKPGPQGPSGDPGPPGPPGKEGLPGP  540
             AGERGPIGPAGPPGERGGKGSKGSQGPKGSRGSPGKPGPQGPSGDPGPPGPPGKEGLPGP
Sbjct:  481  AGERGPIGPAGPPGERGGKGSKGSQGPKGSRGSPGKPGPQGPSGDPGPPGPPGKEGLPGP  540

Query:  541  QGPPGFQGLQGTVGEPGVPGPRGLPGLPGVPGMPGPKGPPGPPGPSGAVVPLALQNEPTP  600
             QGPPGFQGLQGTVGEPGVPGPRGLPGLPGVPGMPGPKGPPGPPGPSGAVVPLALQNEPTP
Sbjct:  541  QGPPGFQGLQGTVGEPGVPGPRGLPGLPGVPGMPGPKGPPGPPGPSGAVVPLALQNEPTP  600

Query:  601  APEDNGCPPHWKNFTDKCYYFSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVG  660
             APEDN CPPHWKNFTDKCYYFSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVG
Sbjct:  601  APEDNSCPPHWKNFTDKCYYFSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVG  660

Query:  661  RESHWIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDCAGLIYAGQWNDF  720
             RESHWIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDCAGLIYAGQWNDF
Sbjct:  661  RESHWIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDCAGLIYAGQWNDF  720

Query:  721  QCEDVNNFICEKDRETVLSSAL  742
             QCEDVNNFICEKDRETVLSSAL
Sbjct:  721  QCEDVNNFICEKDRETVLSSAL  742
```

```
CPU time:       0.13 user secs.        0.06 sys. secs        0.19 total secs.

Lambda      K        H
   0.312     0.133     0.393

Gapped
Lambda    K        H
   0.267   0.0410     0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 19,823
Number of Sequences: 0
Number of extensions: 537
Number of successful extensions: 99
Number of sequences better than 300.0: 1
Number of HSP's better than 300.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 742
length of database: 455,821,981
effective HSP length: 135
effective length of query: 607
effective length of database: 455,821,846
effective search space: 276683860522
effective search space used: 276683860522
T: 9
A: 40
X1: 16 ( 7.2 bits)
X2: 129 (49.7 bits)
```

```
X3: 129 (49.7 bits)
S1: 42  (21.8 bits)
S2: 66  (30.0 bits)
```

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[General] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

General information about the entry

Entry name	**CL43_BOVIN**
Primary accession number	**P42916**
Secondary accession number	Q8WMF4
Entered in Swiss-Prot in	Release 32, November 1995
Sequence was last modified in	Release 41, February 2003
Annotations were last modified in	Release 42, September 2003

Name and origin of the protein

Protein name	**Collectin-43 [Precursor]**
Synonyms	**CL-43**
	43 kDa collectin
Gene name	**CL43**
From	Bos taurus (Bovine) [TaxID: 9913]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.

References

[1] SEQUENCE FROM NUCLEIC ACID.
   TISSUE=Liver;
   MEDLINE=22414671; PubMed=12527419; [NCBI, ExPASy, EBI, Israel, Japan]
   Hansen S., Holm D., Moeller V., Vitved L., Bendixen C., Skjoedt K., Holmskov U.;
   "Genomic and molecular characterization of CL-43 and its proximal promoter.";
   Biochim. Biophys. Acta 1625:1-10(2003).

[2] SEQUENCE OF 21-321 FROM NUCLEIC ACID, AND PARTIAL SEQUENCE.
   TISSUE=Liver;
   MEDLINE=94216283; PubMed=8163480; [NCBI, ExPASy, EBI, Israel, Japan]
   Lim B.-L., Willis A.C., Reid K.B.M., Lu J., Laursen S.B., Jensenius J.C., Holmskov U.;
   "Primary structure of bovine collectin-43 (CL-43). Comparison with conglutinin and lung surfactant protein-D.";
   J. Biol. Chem. 269:11820-11824(1994).

Comments

- *FUNCTION*: LECTIN THAT BINDS TO VARIOUS SUGARS: MANNOSE = MANNAC > FUCOSE > GLCNAC > GLUCOSE = MALTOSE > GALACTOSE > LACTOSE > GALNAC. COULD PLAY A ROLE IN IMMUNE DEFENSE.

- **_SUBUNIT_**: OLIGOMERIC COMPLEX OF 4 SET OF HOMOTRIMERS.
- **_SUBCELLULAR LOCATION_**: Secreted.
- **_TISSUE SPECIFICITY_**: Liver-specific.
- **_PTM_**: Hydroxylated _(Potential)_.
- **_SIMILARITY_**: Contains 1 collagenous domain.
- **_SIMILARITY_**: Contains 1 C-type lectin family domain.

Copyright

Cross-references

EMBL	AY071821; AAL61855.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AY071822; AAL61856.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	X75912; CAA53511.1; ALT_SEQ.	[EMBL / GenBank / DDBJ] [CoDingSequence]
HSSP	P35247; 1B08. [HSSP ENTRY / PDB]	
InterPro	IPR000087; Collagen.	
	IPR001304; Lectin_C.	
	Graphical view of domain structure.	
Pfam	PF00059; lectin_c; 1.	
	PF01391; Collagen; 2.	
SMART	SM00034; CLECT; 1.	
PROSITE	PS00615; C_TYPE_LECTIN_1; 1.	
	PS50041; C_TYPE_LECTIN_2; 1.	
ProDom	[Domain structure / List of seq. sharing at least 1 domain].	
BLOCKS	P42916.	
ProtoNet	P42916.	
ProtoMap	P42916.	
PRESAGE	P42916.	
DIP	P42916.	
ModBase	P42916.	
SWISS-2DPAGE	Get region on 2D PAGE.	

Keywords

Lectin; **Hydroxylation**; **Glycoprotein**; **Mannose-binding**; **Collagen**; **Repeat**; **Calcium**; **Signal**.
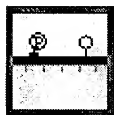
Features

Feature table viewer   Feature aligner

Key	From	To	Length	Description
SIGNAL	1	20	20	
CHAIN	21	321	301	COLLECTIN-43.
DOMAIN	49	162	114	COLLAGEN-LIKE.
DOMAIN	222	321	100	C-TYPE LECTIN (SHORT FORM).
DISULFID	224	319		_BY SIMILARITY._
DISULFID	297	311		_BY SIMILARITY._
CONFLICT	125	125		T -> A (IN REF. 2).
CONFLICT	286	286		N -> G (IN REF. 2).

Sequence information

Length: **321 AA** [This is the length of the unprocessed precursor]

Molecular weight: **33615 Da** [This is the MW of the unprocessed precursor]

CRC64: **12BF120BB48861A1** [This is a checksum on the sequence]

```
            10         20         30         40         50         60
             |          |          |          |          |          |
        MLPLPLSILL LLTQSQSFLG EEMDVYSEKT LTDPCTLVVC APPADSLRGH DGRDGKEGPQ

            70         80         90        100        110        120
             |          |          |          |          |          |
        GEKGDPGPPG MPGPAGREGP SGRQGSMGPP GTPGPKGEPG PEGGVGAPGM PGSPGPAGLK

           130        140        150        160        170        180
             |          |          |          |          |          |
        GERGTPGPGG AIGPQGPSGA MGPPGLKGDR GDPGEKGARG ETSVLEVDTL RQRMRNLEGE

           190        200        210        220        230        240
             |          |          |          |          |          |
        VQRLQNIVTQ YRKAVLFPDG QAVGEKIFKT AGAVKSYSDA EQLCREAKGQ LASPRSSAEN

           250        260        270        280        290        300
             |          |          |          |          |          |
        EAVTQLVRAK NKHAYLSMND ISKEGKFTYP TGGSLDYSNW APGEPNNRAK DEGPENCLEI

           310        320
             |          |
        YSDGNWNDIE CREERLVICE F
```

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Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

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NicePprot View of
Swiss-Prot: Q8MHZ9 [Printer-friendly view] [Quick BlastP search]

[General] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

General information about the entry

Entry name	**CL46_BOVIN**
Primary accession number	**Q8MHZ9**
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 41, February 2003
Sequence was last modified in	Release 41, February 2003
Annotations were last modified in	Release 41, February 2003

Name and origin of the protein

Protein name	**Collectin-46 [Precursor]**
Synonyms	**CL-46**
	46 kDa collectin
Gene name	**CL46**
From	Bos taurus (Bovine) [TaxID: 9913]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.

References

[1] SEQUENCE FROM NUCLEIC ACID.
Hansen S., Holm D., Moeller V., Vitved L., Bendixen C., Reid K.B.M., Skjoedt K., Holmskov U.;
"CL-46, a novel collectin highly expressed in the bovine thymus and liver.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

Comments

- *SUBUNIT*: Oligomeric complex of 4 set of homotrimers *(By similarity)*.
- *SUBCELLULAR LOCATION*: Secreted.
- *TISSUE SPECIFICITY*: Highly expressed in thymus and liver.
- *PTM*: Hydroxylated *(Potential)*.
- *SIMILARITY*: Contains 1 collagenous domain.
- *SIMILARITY*: Contains 1 C-type lectin family domain.

Copyright

Cross-references

AF509589; AAM34742.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]

EMBL	AF509590; AAM34743.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
InterPro	IPR000087; Collagen.
	IPR001304; Lectin_C.
	Graphical view of domain structure.
Pfam	PF00059; lectin_c; 1.
	PF01391; Collagen; 3.
SMART	SM00034; CLECT; 1.
PROSITE	PS00615; C_TYPE_LECTIN_1; 1.
	PS50041; C_TYPE_LECTIN_2; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain].
BLOCKS	Q8MHZ9.
ProtoNet	Q8MHZ9.
ProtoMap	Q8MHZ9.
PRESAGE	Q8MHZ9.
DIP	Q8MHZ9.
ModBase	Q8MHZ9.
SWISS-2DPAGE	Get region on 2D PAGE.

Keywords

Lectin; **Hydroxylation**; **Glycoprotein**; **Mannose-binding**; **Membrane**; **Collagen**; **Repeat**; **Calcium**; **Signal**.
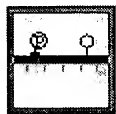
Features

Feature table viewer   Feature aligner
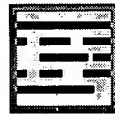
Key	From	To	Length	Description
SIGNAL	1	20	20	*POTENTIAL*.
CHAIN	21	371	351	COLLECTIN-46.
DOMAIN	46	216	171	COLLAGEN-LIKE.
DOMAIN	273	371	99	C-TYPE LECTIN (SHORT FORM).
SITE	201	203	3	CELL ATTACHMENT SITE (*POTENTIAL*).
DISULFID	275	369		*BY SIMILARITY*.
DISULFID	347	361		*BY SIMILARITY*.
CARBOHYD	90	90		N-LINKED (GLCNAC...) (*POTENTIAL*).

Sequence information

Length: **371 AA** [This is the length of the unprocessed precursor]

Molecular weight: **37445 Da** [This is the MW of the unprocessed precursor]

CRC64: **108AC45A91420E83** [This is a checksum on the sequence]

```
            10         20         30         40         50         60
             |          |          |          |          |          |
        MLLLPLSVLL LLTQPWRSLG AEMKIYSQKT LANGCTLVVC RPPEGGLPGR DGQDGREGPQ

            70         80         90        100        110        120
             |          |          |          |          |          |
        GEKGDPGSPG PAGRAGRPGP AGPIGPKGDN GSAGEPGPKG DTGPPGPPGM PGPAGREGPS

           130        140        150        160        170        180
             |          |          |          |          |          |
        GKQGSMGPPG TPGPKGDTGP KGGMGAPGMQ GSPGPAGLKG ERGAPGELGA PGSAGVAGPA
```

```
          190         200         210          220         230         240
           |           |           |            |           |           |
        GAIGPQGPSG ARGPPGLKGD RGDPGERGAK  GESGLADVNA LKQRVTILEG QLQRLQNAFS

          250         260         270          280         290         300
           |           |           |            |           |           |
        RYKKAVLFPD GQAVGKKIFK TAGAVKSYSD  AQQLCREAKG QLASPRSAAE NEAVAQLVRA

          310         320         330          340         350         360
           |           |           |            |           |           |
        KNNDAFLSMN DISTEGKFTY PTGESLVYSN  WASGEPNNNN AGQPENCVQI YREGKWNDVP

          370
           |
        CSEPLLVICE F
```

Q8MHZ9 in
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BLAST BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

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